

SEQUENCE LISTING

<110> ACHEN, Marc G.
STACKER, Steven A.

<120> METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY VASCULAR
ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING FOR NEOPLASTIC
DISEASE OR METASTATIC RISK AND FOR MAINTAINING VASCULARIZATION OF TISSUE

<130> 1064/48666PC

<140> to be assigned

<141> 2001-09-20

<150> 09/796,714

<151> 2001-03-02

<150> 60/234,196

<151> 2000-09-20

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 2029

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (411)..(1472)

<223>

<400> 1

gttgggttcc agctttctgt agctgtaagc attggtggcc acaccacctc cttacaaagc 60

aactagaacc tgcggcatac attggagaga tttttttaat tttctggaca tgaagtaaatt 120

ttagagtgtt ttctaatttc aggtagaaga catgtccacc ttctgattat ttttggagaa 180

catttttgatt tttttcatct ctctctcccc acccctaaga ttgtgcaaaa aaagcgtacc 240

ttgcctaatt gaaataattt cattggattt tgatcagaac tgattatttg gttttctgtg 300

tgaagttttg aggtttcaaa ctttccttct ggagaatgcc ttttgaaaca attttctcta 360

gctgcctgat gtcaactgct tagtaatcag tggatattga aatattcaaa atg tac 416

Met Tyr

1

aga gag tgg gta gtg gtg aat gtt ttc atg atg ttg tac gtc cag ctg 464

Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val Gln Leu

5

10

15

gtg cag ggc tcc agt aat gaa cat gga cca gtg aag cga tca tct cag 512

Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser Ser Gln

20

25

30

tcc aca ttg gaa cga tct gaa cag cag atc agg gct gct tct agt ttg	560
Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser Ser Leu	
35 40 45 50	
gag gaa cta ctt cga att act cac tct gag gac tgg aag ctg tgg aga	608
Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu Trp Arg	
55 60 65	
tgc agg ctg agg ctc aaa agt ttt acc agt atg gac tct cgc tca gca	656
Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg Ser Ala	
70 75 80	
tcc cat cgg tcc act agg ttt gcg gca act ttc tat gac att gaa aca	704
Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile Glu Thr	
85 90 95	
cta aaa gtt ata gat gaa gaa tgg caa aga act cag tgc agc cct aga	752
Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser Pro Arg	
100 105 110	
gaa acg tgc gtg gag gtg gcc agt gag ctg ggg aag agt acc aac aca	800
Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr Asn Thr	
115 120 125 130	
ttc ttc aag ccc cct tgt gtg aac gtg ttc cga tgt ggt ggc tgt tgc	848
Phe Phe Lys Pro Cys Val Asn Val Phe Arg Cys Gly Gly Cys Cys	
135 140 145	
aat gaa gag agc ctt atc tgt atg aac acc agc acc tcg tac att tcc	896
Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr Ile Ser	
150 155 160	
aaa cag ctc ttt gag ata tca gtg cct ttg aca tca gta cct gaa tta	944
Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro Glu Leu	
165 170 175	
gtg cct gtt aaa gtt gcc aat cat aca ggt tgt aag tgc ttg cca aca	992
Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu Pro Thr	
180 185 190	
gcc ccc cgc cat cca tac tca att atc aga aga tcc atc cag atc cct	1040
Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln Ile Pro	
195 200 205 210	
gaa gaa gat cgc tgt tcc cat tcc aag aaa ctc tgt cct att gac atg	1088
Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile Asp Met	
215 220 225	
cta tgg gat agc aac aaa tgt aaa tgt gtt ttg cag gag gaa aat cca	1136
Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu Asn Pro	
230 235 240	
ctt gct gga aca gaa gac cac tct cat ctc cag gaa cca gct ctc tgt	1184
Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala Leu Cys	
245 250 255	
ggg cca cac atg atg ttt gac gaa gat cgt tgc gag tgt gtc tgt aaa	1232
Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val Cys Lys	
260 265 270	

aca cca tgt ccc aaa gat cta atc cag cac ccc aaa aac tgc agt tgc	1280
Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys Ser Cys	
275 280 285 290	
ttt gag tgc aaa gaa agt ctg gag acc tgc tgc cag aag cac aag cta	1328
Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His Lys Leu	
295 300 305	
ttt cac cca gac acc tgc agc tgt gag gac aga tgc ccc ttt cat acc	1376
Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe His Thr	
310 315 320	
aga cca tgt gca agt ggc aaa aca gca tgt gca aag cat tgc cgc ttt	1424
Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys Arg Phe	
325 330 335	
cca aag gag aaa agg gct gcc cag ggg ccc cac agc cga aag aat cct	1472
Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys Asn Pro	
340 345 350	
tgattcagcg ttccaagttc cccatccctg tcatttttaa cagcatgctg ctttgccaag	1532
ttgctgtcac tgtttttttc ccaggtgtta aaaaaaaaaat ccattttaca cagcaccaca	1592
gtgaatccag accaaccttc cattcacacc agctaaggag tccctgggtc attgatggat	1652
gtgttctagc tgcagatgcc tctgcgacc aaggaatgga gaggagggga cccatgtaat	1712
ccttttgttt agttttgttt ttgttttttg gtgaatgaga aaggtgtgct ggtcatggaa	1772
tggcaggtgt catatgactg attactcaga gcagatgagg aaaactgtag tctctgagtc	1832
ctttgctaatt cgcaactctt gtgaattatt ctgattcttt tttatgcaga atttgattcg	1892
tatgatcagt actgactttc tgattactgt ccagcttata gtcttccagt ttaatgaact	1952
accatctgat gtttcatatt taagtgtatt taaagaaaat aaacaccatt attcaagcca	2012
aaaaaaaaaa aaaaaaa	2029

<210> 2
 <211> 354
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Tyr Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val
1 5 10 15

Gln Leu Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser
20 25 30

Ser Gln Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
35 40 45

Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
50 55 60

Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
65 70 75 80

Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
85 90 95

Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
100 105 110

Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
115 120 125

Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
130 135 140

Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr
145 150 155 160

Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro
165 170 175

Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu
180 185 190

Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln
195 200 205

Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile
210 215 220

Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu
225 230 235 240

Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala
245 250 255

Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val
260 265 270

Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys
275 280 285

Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His
 290 295 300

Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe
 305 310 315 320

His Thr Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys
 325 330 335

Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys
 340 345 350

Asn Pro

<210> 3
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 3

Phe Tyr Asp Ile Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg
 1 5 10 15

Thr Gln Cys Ser Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu
 20 25 30

Gly Lys Ser Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe
 35 40 45

Arg Cys Gly Gly Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr
 50 55 60

Ser Thr Ser Tyr Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu
 65 70 75 80

Thr Ser Val Pro Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly
 85 90 95

Cys Lys Cys Leu Pro Thr Ala Pro Arg His Pro Tyr Ser
 100 105

<210> 4
 <211> 1325
 <212> DNA
 <213> Murinae gen. sp.

<400> 4
 ggagaatgcc ttttgcaaca cttttcagta gctgcctgga aacaactgct tagtcatcgg 60
 tagacattta aaatattcaa aatgtatgga gaatggggaa tggggaatat cctcatgatg 120
 ttccatgtgt acttggtgca gggcttcagg agcgaacatg gaccagtga ggaatttttct 180
 tttgagcgat catccccgtc catgttgga cgatctgaac aacagatccg agcagcttct 240
 agtttgagg agttgctgca aatcgcgcac tctgaggact ggaagctgtg gcgatgccgg 300
 ttgaagctca aaagtcttgc cagtatggac tcacgctcag catcccatcg ctccaccaga 360
 tttgcggcaa ctttctatga cactgaaaca ctaaaagtta tagatgaaga atggcagagg 420
 acccaatgca gccctagaga gacatgcgta gaagtcgcca gtgagctggg gaagacaacc 480
 aacacattct tcaagcccc ctgtgtaaat gtcttccggt gtggaggctg ctgcaacgaa 540
 gaggggtgtga tgtgtatgaa cacaagcacc tcctacatct ccaaacagct ctttgagata 600
 tcagtgcctc tgacatcagt gcccagagta gtgcctgtta aaattgccaa ccatacgggt 660
 tgtaagtgtc tgcccacggg cccccgcat ccttactcaa ttatcagaag atccattcag 720
 accccagaag aagatgaatg tcctcattcc aagaaactct gtcctattga catgctgtgg 780
 gataacacca aatgtaaatg tgttttgcaa gacgagactc cactgcctgg gacagaagac 840
 cactcttacc tccaggaacc cactctctgt ggaccgcaca tgacgtttga tgaagatcgc 900
 tgtgagtgcg tctgtaaagc accatgtccg ggagatctca ttcagcacc ggaaaactgc 960
 agttgctttg agtgcaaaga aagtctggag agctgctgcc aaaagcacia gatttttcac 1020
 ccagacacct gcagctgtga ggacagatgt ctttttcaca ccagaacatg tgcaagtaga 1080
 aagccagcct gtggaaagca ctggcgcttt ccaaaggaga caagggccca gggactctac 1140
 agccaggaga acccttgatt caacttcctt tcaagtcacc ccactctctgt cattttaaac 1200
 agctcactgc tttgtcaagt tgctgtcact gttgcccact accccttgaa catgtgcaaa 1260
 cacagacaca cacacacaca cacacacaga gcaactagaa ttatgttttc taggtgctgc 1320
 ctaag 1325